

GenCore version 4.5
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AM nucleotide - nucleotide search, using SW model

Run on: February 26, 2002, 16:17:03 / Search time: 274.41 seconds
(without alignments)
11595.897 Million CPU seconds

Title: US-09-576-778-9

Percent score: 1941

Sequences: 1 atgaagacgacatcatttggac.....gacatgacacatctatctat 1941

Scoring table:

Gapop: 10.0 / Repeat: 1.0

Searched: 1472140 seqs, 824878755 matches

Minimum DB seq length: 9

Maximum DB seq length: 295020000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database:

1:	gb_bat*
2:	gb_bat*
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35:	gb_bat*
36:	gb_bat*

Prod. No. is the number of results predicted by BLAST to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the local score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1282.4	66.1	2124	1	AF180561	AF180561 Myxobacter
2	792.4	42.1	485	1	AF206716	AF206716 Bacillus
3	751.2	38.7	285	1	AF0004098	AF0004098 Bacillus
4	702.6	36.2	266	6	B61428	B61428 DNA sequence
5	669	21.4	1461	1	EF014614	EF014614 Bacillus
6	507.2	26.1	1469	1	CF0802	CF0802 Myxobacter
7	490.2	25.1	1019	1	CF0802	CF0802 Myxobacter
8	476.4	24.5	561	1	AF086105	AF086105 Myxobacter
9	466.6	24.0	4652	1	CF0802	CF0802 Myxobacter
10	464.6	23.9	7534	1	CF0802	CF0802 Myxobacter
11	462.8	23.8	2590	1	CF0802	CF0802 Myxobacter
12	417.8	23.1	5739	1	CF0802	CF0802 Myxobacter
13	412.6	22.1	5681	1	CF0802	CF0802 Myxobacter
14	404.4	20.8	1469	1	AF086105	AF086105 Myxobacter
15	397.9	20.0	2951	1	CF0802	CF0802 Myxobacter
16	386.6	19.9	6805	1	AF086105	AF086105 Myxobacter
17	386.6	19.9	6805	1	AF086105	AF086105 Myxobacter
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19	346	17.8	4856	1	CF0802	CF0802 Myxobacter
20	328.2	16.9	1701	1	CF0802	CF0802 Myxobacter
21	311.6	16.1	2839	1	AF086105	AF086105 Myxobacter
22	294.6	15.2	3830	1	CF0802	CF0802 Myxobacter
23	260.8	13.4	1132	1	AF086105	AF086105 Myxobacter
24	250.6	13.4	1655	1	CF0802	CF0802 Myxobacter
25	217.6	12.0	1461	1	CF0802	CF0802 Myxobacter
26	245	12.6	1660	1	AF086105	AF086105 Myxobacter
27	241	12.6	1447	1	AF086105	AF086105 Myxobacter
28	244	12.6	1447	1	AF086105	AF086105 Myxobacter
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31	212.4	12.5	1447	1	AF086105	AF086105 Myxobacter
32	242	12.5	1447	1	AF086105	AF086105 Myxobacter
33	247.4	12.2	4713	1	AF086105	AF086105 Myxobacter
34	246.8	12.2	2622	1	AF086105	AF086105 Myxobacter
35	243.8	12.3	2634	1	AF086105	AF086105 Myxobacter
36	241.4	11.9	1685	1	AF086105	AF086105 Myxobacter
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38	231.2	11.9	1685	1	AF086105	AF086105 Myxobacter
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40	226.4	11.7	1466	1	AF086105	AF086105 Myxobacter
41	225.9	11.6	1466	1	AF086105	AF086105 Myxobacter
42	224	11.5	810	1	AF086105	AF086105 Myxobacter
43	216	11.1	2483	1	AF086105	AF086105 Myxobacter
44	214.4	11.0	2502	1	AF086105	AF086105 Myxobacter
45	209.2	10.8	11871	2	AF086105	AF086105 Myxobacter

ALIGNMENTS

Result	Accession	Version	RevWords	Source	Organism	Ref
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36	AF180561			Myxobacter sp. AT-1	Myxobacter sp. AT-1	22 FEB-2000

REFERENCES

1. (Accession 2124) bp DNA
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78	87.101E-1.9997	9908.01436.88
79	88.101E-1.9997	9908.01436.88
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81	90.101E-1.9997	9908.01436.88
82	91.101E-1.9997	9908.01436.88
83	92.101E-1.9997	9908.01436.88
84	93.101E-1.9997	9908.01436.88
85	94.101E-1.9997	9908.01436.88
86	95.101E-1.9997	9908.01436.88
87	96.101E-1.9997	9908.01436.88
88	97.101E-1.9997	9908.01436.88
89	98.101E-1.9997	9908.01436.88
90	99.101E-1.9997	9908.01436.88
91		

PR	26	001	1999	9605	01	01	00																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												</
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F6	2.7	AlO ₃	1.9999	9.9085-01.51.06.6.
F6	2.7	AlO ₃	1.9999	9.9085-01.51.08.0.
F6	4.0	AlO ₃	1.9999	9.9085-01.51.18.3.
F6	3.1	AlO ₃	1.9999	9.9085-01.51.4.48.
F6	0.1	SiEP	1.9999	9.9085-01.51.19.30.
F6	0.7	SiEP	1.9999	9.9085-01.5.2.86.8.
F6	1.9	SiEP	1.9999	9.9085-01.5.33.72.
F6	1.3	SiEP	1.9999	9.9085-01.5.37.58.
F6	1.5	SiEP	1.9999	9.9085-01.5.40.78.
F6	1.6	SiEP	1.9999	9.9085-01.5.40.39.
F6	2.0	SiEP	1.9999	9.9085-01.5.47.79.
F6	2.2	SiEP	1.9999	9.9085-01.5.51.39.
F6	2.3	SiEP	1.9999	9.9085-01.5.54.86.
F6	2.4	SiEP	1.9999	9.9085-01.5.56.59.
F6	2.6	SiEP	1.9999	9.9085-01.5.6.4.58.
F6	2.9	SiEP	1.9999	9.9085-01.5.6.59.6.
F6	0.4	SiEP	1.9999	9.9085-01.5.7.1.7.
F6	0.5-0.8.1	1.9999	9.9085-01.5.7.7.5.	
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F6	1.3-0.8.1	1.9999	9.9085-01.5.9.2.9.6.	
F6	1.4-0.8.1	1.9999	9.9085-01.5.9.3.2.9.	
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F6	1.4-0.8.1	1.9999	9.9085-01.5.9.6.3.7.	
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F6	2.1-0.8.1	1.9999	9.9085-01.6.0.7.4.1.	
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F6	2.1-0.8.1	1.9999	9.9085-01.6.0.7.6.8.	
F6	2.1-0.8.1	1.9999	9.9085-01.6.0.7.7.0.	
F6	2.1-0.8.1	1.9999	9.9085-01.6.0.8.1.4.	
F6	2.1-0.8.1	1.9999	9.9085-01.6.0.8.1.5.	
F6	2.2-0.8.1	1.9999	9.9085-01.6.0.9.8.0.	
F6	2.2-0.8.1	1.9999	9.9085-01.6.0.9.8.1.	
F6	2.2-0.8.1	1.9999	9.9085-01.6.0.9.8.3.	
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F6	2.6-0.8.1	1.9999	9.9085-01.6.1.8.6.0.	
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F6	2.6-0.8.1	1.9999	9.9085-01.6.1.9.2.0.	
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F6	2.9-0.8.1	1.9999	9.9085-01.6.2.1.4.2.	

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III. Interactions of ESIs from significant predators
 (published 2006)
 Contact: Cathy Konrad

[illegible]

Search completed: February 26, 2002, 16:50:32
Job time: 9386 sec



Query Match 19,989 Score 196.6 E-4 Length 6416
 Host Local Similarity 52.5% Read No. 156122
 Matches 9481 Conserved 07 Mismatches 8492 Indels 481 Gaps 41

55 TTTTCTGGAAGAGCGCTGGAGCTTCTGGTGAAGATATCTCTGATATATGATCTG 114
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 1b CTATATGAAGCAATATATGCTTATGATCTTCATATGTCAGAGCAAGCTTACTTCTGCGGTA 825
 59 175 CAGTGAATCTGAAGAGAGCTCTGAGCTTGAAGAGAGAGAGAGCTCTGAGCTCTG 234
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59 1075 GTTATCTGAG 1134
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 59 1915 GAG 1974
 1b 2518 GATAG 2574

RESULT 2

US-08-635-066-1

Sequence 1: Affiliation US/0865066

Patient No. 5945580

STRAB. 16-05-01-01-01

APPLICANT: Janssen, Pamela

APPLICANT: Haffner, Mark H.

TITLE OF INVENTION: Capsicum, Hot/Pepper, Polynoidolides

TITLE OF INVENTION: and Polynoidolides

NUMBER OF SEQUENCES: 8

ORIGIN: NIDDK, Bethesda

PR 14 MAY 1999; 9905-0134421.
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OM Protein: protein search, using SW model

Run on: February 26, 2002, 11:45:46 : Search time 14.57 seconds
(without alignments)
1771.579 hits (0.11 update/2500)

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Percent score: 08.09 576 728 76
Sequence: 1 MKALGALVATVSEIASLS.....LSTLYVARKLV-RRPQY 616

Scoring table:
Gapop 10.0, Gapext 0.5

Searches: 100059 seqs, 666487 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 6

Maximum DB seq length: 200000000

Post-processing: Maximum Match OK

Database: SwissProt_43_*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the observed one, given a fixed product, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2811.5	66.1	646	G0N4_BACSC	P25622 bacillus sp
2	1957.5	56.0	679	G0N4_BACSC	P25622 bacillus sp
3	1869	53.4	986	G0N4_BACSC	P25622 bacillus sp
4	1812	51.8	1242	G0N4_BACSC	P25622 bacillus sp
5	1773.5	50.7	725	G0N4_BACSC	P25622 bacillus sp
6	1749.5	50.0	840	G0N4_BACSC	P25622 bacillus sp
7	1738	49.2	779	G0N4_BACSC	P25622 bacillus sp
8	1664.5	47.6	1045	G0N4_BACSC	P25622 bacillus sp
9	1083.5	31.0	705	G0N4_BACSC	P25622 bacillus sp
10	821.5	23.5	496	G0N4_BACSC	P25622 bacillus sp
11	816	23.2	494	G0N4_BACSC	P25622 bacillus sp
12	792	21.7	451	G0N4_BACSC	P25622 bacillus sp
13	446	9.9	746	G0N4_BACSC	P25622 bacillus sp
14	297.5	8.2	962	G0N4_BACSC	P25622 bacillus sp
15	279	8.0	1101	G0N4_BACSC	P25622 bacillus sp
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17	199	5.7	547	G0N4_BACSC	P25622 bacillus sp
18	175.5	5.0	140	G0N4_BACSC	P25622 bacillus sp
19	157.5	4.5	700	G0N4_BACSC	P25622 bacillus sp
20	142	4.1	411	G0N4_BACSC	P25622 bacillus sp
21	125.5	3.6	1246	G0N4_BACSC	P25622 bacillus sp
22	123.5	3.5	1409	G0N4_BACSC	P25622 bacillus sp
23	123.5	3.5	1415	G0N4_BACSC	P25622 bacillus sp
24	123	3.5	1415	G0N4_BACSC	P25622 bacillus sp
25	117	3.4	908	G0N4_BACSC	P25622 bacillus sp
26	115	3.3	499	G0N4_BACSC	P25622 bacillus sp
27	114	3.3	499	G0N4_BACSC	P25622 bacillus sp
28	114	3.3	499	G0N4_BACSC	P25622 bacillus sp
29	114	3.3	499	G0N4_BACSC	P25622 bacillus sp
30	110.5	3.2	702	G0N4_BACSC	P25622 bacillus sp
31	110	3.1	802	G0N4_BACSC	P25622 bacillus sp
32	109	3.1	802	G0N4_BACSC	P25622 bacillus sp
33	108.5	3.1	1331	G0N4_BACSC	P25622 bacillus sp

ALIGNMENTS

Result No.	Score	Match	Length	ID	Description
1	2811.5	66.1	646	G0N4_BACSC	P25622 bacillus sp
2	1957.5	56.0	679	G0N4_BACSC	P25622 bacillus sp
3	1869	53.4	986	G0N4_BACSC	P25622 bacillus sp
4	1812	51.8	1242	G0N4_BACSC	P25622 bacillus sp
5	1773.5	50.7	725	G0N4_BACSC	P25622 bacillus sp
6	1749.5	50.0	840	G0N4_BACSC	P25622 bacillus sp
7	1738	49.2	779	G0N4_BACSC	P25622 bacillus sp
8	1664.5	47.6	1045	G0N4_BACSC	P25622 bacillus sp
9	1083.5	31.0	705	G0N4_BACSC	P25622 bacillus sp
10	821.5	23.5	496	G0N4_BACSC	P25622 bacillus sp
11	816	23.2	494	G0N4_BACSC	P25622 bacillus sp
12	792	21.7	451	G0N4_BACSC	P25622 bacillus sp
13	446	9.9	746	G0N4_BACSC	P25622 bacillus sp
14	297.5	8.2	962	G0N4_BACSC	P25622 bacillus sp
15	279	8.0	1101	G0N4_BACSC	P25622 bacillus sp
16	240	6.9	649	G0N4_BACSC	P25622 bacillus sp
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19	157.5	4.5	700	G0N4_BACSC	P25622 bacillus sp
20	142	4.1	411	G0N4_BACSC	P25622 bacillus sp
21	125.5	3.6	1246	G0N4_BACSC	P25622 bacillus sp
22	123.5	3.5	1409	G0N4_BACSC	P25622 bacillus sp
23	123.5	3.5	1415	G0N4_BACSC	P25622 bacillus sp
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25	117	3.4	908	G0N4_BACSC	P25622 bacillus sp
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27	114	3.3	499	G0N4_BACSC	P25622 bacillus sp
28	114	3.3	499	G0N4_BACSC	P25622 bacillus sp
29	114	3.3	499	G0N4_BACSC	P25622 bacillus sp
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31	110	3.1	802	G0N4_BACSC	P25622 bacillus sp
32	109	3.1	802	G0N4_BACSC	P25622 bacillus sp
33	108.5	3.1	1331	G0N4_BACSC	P25622 bacillus sp

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 12 01 MAY 1997 (TERMINAL, 03, updated)
 13 01 MAY 1997 (TERMINAL, 03, last sequence updated)
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10 PROSIT 1711 AA
 11 PROSIT 1711 AA
 12 01 MAY 1997 (TERMINAL, 03, updated)
 13 01 MAY 1997 (TERMINAL, 03, last sequence updated)
 14 01 JUN 2001 (TERMINAL, 17, last sequence updated)
 15 ERGONOMICS A (03, last sequence updated)
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1 CHERSE RANCH ADDRESS
 2 ADDRESS: Townsend and Townsend and crew
 3 STREET: 700 Market Street, Suite 100
 4 CITY: San Francisco
 5 STATE: California
 6 COUNTRY: USA
 7 ZIP: 94105-1192
 8
 9 MOTION PICTURE FORM
 10 MOTION TYPE: Floppy disk
 11 COMPUTER: IBM PC compatible
 12 OPERATING SYSTEM: PC 2.296 MS
 13 SOFTWARE: Patented Release #1.0, Version #1.0
 14 CURRENT APPLICATION DATA:
 15 APPLICATION NUMBER: 07/06/27/11-417
 16 FILING DATE: 04-MAY 1995
 17 CLASSIFICATION: 546
 18 PRIOR APPLICATION DATA:
 19 APPLICATION NUMBER: 07/06/27/11-417
 20 FILING DATE: 07-JUL-1994
 21 PRIOR APPLICATION DATA:
 22 APPLICATION NUMBER: 07/07/07/11-417
 23 FILING DATE: 19-APR-1991
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: 07/07/11-417
 26 FILING DATE: 20-APR 1990
 27 ATTORNEY/AGENT INFORMATION:
 28 NAME: Easton, Kevin L.
 29 REGISTRATION NUMBER: 44,774
 30 REFERENCE/AGENT NUMBER: 023078 04/09/95
 31 TELEPHONE: (415) 543-9600
 32 TELEFAX: (415) 543-9647
 33 INFORMATION FOR SEQ ID NO: 2:
 34 SEQUENCE CHARACTERISTICS:
 35 LENGTH: 901 amino acids
 36 TYPE: amino acid
 37 PROPERTY: linear
 38 MODIFIED TYPE: Prototin
 39 US-09-54-702-2

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